

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 4, 2005, 13:45:23 ; Search time 131 Seconds
(without alignments)
7281.517 Million cell updates/sec

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Title: US-09-640-582A-1
Perfect score: 1342
Sequence: 1 cgttcgcgttcaccaagatc.....cacctgchgcncctcaccc 1342
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database : Issued Patents NA:*
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4: /cgn2_6/prodata/1/ina/6A_COMB_seg.*
5: /cgn2_6/prodata/1/ina/PTCUTS_COMB_seg.*
6: /cgn2_6/prodata/1/ina/backfile1_seg.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1207	89.9	1792	4	US-08-086-336-40	Sequence 40, Appl
2	1194.4	89.0	1790	4	US-09-997-685A-11	Sequence 11, Appl
3	874.2	65.1	1512	4	US-09-086-436-32	Sequence 32, Appl
4	871	64.9	1584	4	US-08-997-685A-3	Sequence 3, Appl
5	751.8	56.0	2976	4	US-09-774-528-317	Sequence 317, Appl
6	735.2	54.8	2733	4	US-08-997-685A-1	Sequence 1, Appl
7	706	52.6	1518	4	US-09-086-436-14	Sequence 34, Appl
8	688.8	51.3	1507	4	US-08-997-685A-5	Sequence 5, Appl
9	680.2	50.7	2246	4	US-09-086-436-38	Sequence 38, Appl
10	680.2	50.7	2263	4	US-08-997-685A-9	Sequence 9, Appl
11	680.2	50.7	3224	4	US-09-774-528-338	Sequence 238, Appl
12	666.6	49.7	1307	3	US-09-172-422-3	Sequence 3, Appl
13	331.8	24.7	1083	4	US-09-270-767-1038	Sequence 1038, Appl
14	331.8	24.7	1083	4	US-09-270-767-16320	Sequence 16320, A
15	123.6	9.2	1040	4	US-09-086-436-36	Sequence 36, Appl
16	110	8.2	1060	4	US-08-997-685A-7	Sequence 7, Appl
17	102.6	7.6	3480	3	US-09-226-012-1	Sequence 1, Appl
18	102.6	7.6	3250	3	US-09-226-012-3	Sequence 3, Appl
19	86.6	6.5	3249	4	US-09-356-383C-3	Sequence 3, Appl
20	86.6	6.5	3355	4	US-09-356-383C-1	Sequence 1, Appl
21	85.4	6.4	3323	3	US-09-600-479-1	Sequence 1, Appl
22	83.8	6.2	3249	4	US-09-343-494-2	Sequence 2, Appl
23	83.8	6.2	3857	4	US-09-336-643A-19	Sequence 19, Appl
24	78.6	5.9	3041	4	US-09-774-177A-19	Sequence 19, Appl
25	70.8	5.3	2366	4	US-09-799-451-351	Sequence 351, Appl
26	63.8	4.8	2241	2	US-08-838-219B-20	Sequence 20, Appl
27	63.8	4.8	2241	3	US-09-233-336A-20	Sequence 20, Appl

ALIGNMENTS

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      28   63.8   4.8   2241    3   US-09-233-752A-20       Sequence 20, Appl
      29   63.8   4.8   2241    3   US-09-402-036A-20       Sequence 20, Appl
      30   63.8   4.8   2241    4   US-09-904-226A-20       Sequence 20, Appl
      31   63.8   4.8   2370    2   US-08-838-219B-19       Sequence 19, Appl
      32   63.8   4.8   2370    3   US-09-233-336A-19       Sequence 19, Appl
      33   63.8   4.8   2370    3   US-09-233-752A-19       Sequence 19, Appl
      34   63.8   4.8   2370    3   US-09-402-036A-19       Sequence 19, Appl
      35   63.8   4.8   2370    4   US-09-904-226A-19       Sequence 19, Appl
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      37   63.8   4.8   2403    2   US-08-471-044A-30       Sequence 30, Appl
      38   63.8   4.8   2403    2   US-08-463-483A-30       Sequence 30, Appl
      39   63.8   4.8   2403    2   US-08-471-046A-30       Sequence 30, Appl
      40   63.8   4.8   2403    2   US-08-470-566B-30       Sequence 30, Appl
      41   63.8   4.8   2403    2   US-08-838-219B-7        Sequence 7, Appl
      42   63.8   4.8   2403    2   US-08-469-334A-30       Sequence 30, Appl
      43   63.8   4.8   2403    3   US-09-300-529A-30       Sequence 30, Appl
      44   63.8   4.8   2403    3   US-09-233-336A-7        Sequence 7, Appl
      45   63.8   4.8   2403    3   US-09-233-752A-7        Sequence 7, Appl


ALIGNMENTS

RESULT 1
US-09-086-436-40
; Sequence 40, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandell, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Barsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Gareth
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 1792
; TYPE: DNA
; ORGANISM: Human
US-09-086-436-40

Query Match          89.9%; Score 1207; DB 4; Length 1792;
Best Local Similarity 99.0%; Pred. No. 3.2e+238;
Matches 1235; Conservative 0; Mismatches 11; Indels 2; Gaps 2
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OM nucleic - nucleic search, using sw model

Run on: January 4, 2005, 13:42:39 ; Search time 5779 Seconds
(without alignments)
10981.619 Million cell updates/sec

Title: US-09-640-582a-1
Sequence: 1 cgttgagcttcacacagatc.....cactgchgcncctcacc 1342
Perfect score: 1342

Scoring table: IDENTITY NUC
Gap 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364489745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: gb_in:*
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5: gb_ov:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1297	96.6	3372	6	AX211346 Sequence
3	1297	96.6	3372	5	AF065164 Homo sapi
4	1295.4	96.5	3459	6	AX348086 Sequence
5	1295.4	96.5	3459	9	HS012582 Homo sapi
6	1208	90.0	1792	9	AF064877 Homo sapi
7	1207	89.9	1792	6	AR483555 Sequence
8	1194.8	89.0	105108	2	AC139689 Homo sapi
9	1194.8	89.0	133193	2	AC139548 Homo sapi
10	1194.8	89.0	199198	9	AC021413 Homo sapi
11	1194.4	89.0	1790	6	AR307665 Sequence
12	1193.4	88.9	127432	2	BD139757 Homo sapi
13	1193.2	88.9	163776	2	AC136294 Homo sapi
14	1192.6	88.8	2125	6	AX647819 Sequence
15	1191.6	88.8	123089	9	AC135731 Homo sapi
16	1191.6	88.8	123089	6	AX647819 Sequence
17	1191.6	88.8	123233	2	AC135625 Homo sapi
18	1191.6	88.8	158033	2	AC135991 Homo sapi
19	1191.6	88.8	164711	2	AC139564 Homo sapi

C	20	1191.6	88.8	166484	2	AC026830 Homo sapi
C	21	1191.6	88.8	184252	2	AC139565 Homo sapi
C	22	1191.6	88.8	184448	9	AC139426 Homo sapi
C	23	1101.2	82.1	1654	6	CO718501 Sequence
C	24	1074.2	80.0	2633	10	AB164197 Rattus no
C	25	1071	79.8	2511	10	AF247451 Rattus no
C	26	1048.6	78.1	3102	6	AX211350 Sequence
C	27	1048.6	78.1	3102	10	MM2225122 Mus muscu
C	28	1032.4	76.9	1820	6	AX018997 Sequence
C	29	996	74.2	1031	9	AF064851 Homo sapi
C	30	992.4	73.9	2866	4	AX019000 Sequence
C	31	953.4	71.0	3737	4	AB022927 Oryctolag
C	32	940.6	70.1	152040	2	AC139547 Homo sapi
C	33	927.2	69.1	4751	6	AX019005 Sequence
C	34	927.2	69.1	4751	6	AX348088 Sequence
C	35	927.2	69.1	4751	9	HS0132429 Homo sapi
C	36	927.2	69.1	5065	9	HS0132429 Homo sapi
C	37	927.2	69.1	5065	9	HS0132429 Homo sapi
C	38	925.6	69.0	4333	6	CO715368 Sequence
C	39	925.6	69.0	4333	6	CO729612 Sequence
C	40	896.8	66.8	3993	10	AF247453 Rattus no
C	41	874.2	65.1	1512	6	AR483551 Sequence
C	42	874.2	65.1	1513	10	AF064873 Mus muscu
C	43	871	64.9	1584	6	AR307661 Homo sapi
C	44	871	64.9	1584	6	BD139756 Ion cham
C	45	763.8	56.9	3053	5	AF421883 Oncorhync

ALIGNMENTS

RESULT 1
LOCUS AX018991 1342 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO942574.
ACCESSION AX018991
VERSION AX018991.1 GI:10043084
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Baumann, A., Gauss, R., Kaupp, B., Boenigk, W., Scholten, A. and Seifert, R.
TITLE Sequences of an ionic channel and the use thereof
JOURNAL Patient: WO 942574-A 1 26-AUG-1999.

WOLFGANG (DE); KAUPP BENJAMIN (DE); BOENIGK ALEXANDER (DE); SEIFERT REINHARD (DE)
FEATURES
source 1..1342
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.5%; Score 1335.6; DB 6; Length 1342;
Best Local Similarity 100.0%; Pred. No. 1.4e-169;
Matches 1342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTTGGCTTACCAAGATCTCAGCTCTCGGCTGCGCCCTCAGCCCTGATCC 60
1 CGTTGGCTTACCAAGATCTCAGCTCTCGGCTGCGCCCTCAGCCCTGATCC 60
61 GCTACATCATAGTGGAGAGATCTTCCACATGACCTATGACCTGGCCAGCGGTGA 120
61 GCTACATCATAGTGGAGAGATCTTCCACATGACCTATGACCTGGCCAGCGGTGA 120
121 TAGGATCTGCATCTCATGAGATGCTGCTCTGCGACCTGGAGCGGCTGCTGC 180
121 TAGGATCTGCATCTCATGAGATGCTGCTCTGCGACCTGGAGCGGCTGCTGC 180

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OM nucleic - nucleic search, using sw model

Run on: January 4, 2005, 13:44:53 ; Search time 705 Seconds
(without alignments)
9992.515 Million cell updates/sec

Title: US-09-640-582a-1

Perfect score: 1342

Sequence: 1 cgttcgctccacacgaatc.....cactcgcgcgcacccaccc 1342

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335.6	99.5	1342	2	AAZ09482 Human Ih
2	1297.6	96.6	3372	2	AAH48729 Human HCN
3	1295.4	96.5	3459	2	AAZ09756 Human HCN
4	1194.4	89.0	1790	2	AAH84445 Human bra
5	1191.6	88.8	2125	10	ADC87558 Human bra
6	1113.2	83.0	3431	4	AAH98302 Human GPC
7	1048.6	78.1	3102	4	AAH48731 Human EST
8	1032.4	76.9	1820	2	AAZ09488 Bovine re
9	992.4	73.9	2886	2	AAZ09491 Human Ih
10	927.2	69.1	4751	2	AAZ09496 Human bra
11	927.2	69.1	4751	6	AAZ09757 Human HCN
12	927.2	69.1	5065	4	AAH48730 Human HCN
13	927.2	69.1	5065	4	AAH48730 Human HCN
14	871.4	64.9	1584	2	AAH84444 Mouse bra
15	753.4	56.1	3852	6	AAH44691 Human tra
16	753.4	56.1	2340	6	ABK6386 Human HCN
17	751.8	56.0	2317	8	ABX71090 Human HCN
18	751.8	56.0	2325	3	AAH6779 Human HCN
19	751.8	56.0	2325	3	ABZ75841 Human HCN
20	751.8	56.0	2325	8	ABZ58682 Human HCN
21	751.8	56.0	2325	8	ACA61916 CDNA enco

22	751.8	56.0	2325	10	ABX95515	ABX95515 CDNA enco
23	751.8	56.0	3496	6	AAZ09758	AAZ09758 Human HCN
24	751.4	56.0	2340	6	ABK6387	ABK6387 Human HCN
25	751.4	56.0	2340	6	ABK6385	ABK6385 Human HCN
26	735.2	54.8	2733	2	AAH84442	AAH84442 Mouse bra
27	720.8	53.7	3112	2	AAZ09483	AAZ09483 Rat Olfac
28	688.8	51.3	1507	2	AAH84446	AAH84446 Mouse bra
29	681.8	50.8	2990	10	ADJ95123	ADJ95123 Novel NOV
30	680.2	50.7	1873	6	AAH18224	AAH18224 Human PCR
31	680.2	50.7	1873	6	AAH18223	AAH18223 Human PCR
32	680.2	50.7	2263	2	AAH84443	AAH84443 Human bra
33	680.2	50.7	2670	6	AAZ09755	AAZ09755 Human HCN
34	680.2	50.7	2673	8	ABZ75836	ABZ75836 Human HCN
35	680.2	50.7	2673	8	ABZ58677	ABZ58677 Human HCN
36	680.2	50.7	2673	8	ACA61911	ACA61911 CDNA enco
37	680.2	50.7	2673	10	ABX95510	ABX95510 CDNA enco
38	680.2	50.7	2748	6	ABT09623	ABT09623 Human HCN
39	680.2	50.7	2748	6	ABT09624	ABT09624 Human HCN
40	680.2	50.7	2748	6	ABT09630	ABT09630 Human HCN
41	680.2	50.7	2748	6	ABT09629	ABT09629 Human HCN
42	680.2	50.7	2748	6	ABT09631	ABT09631 Human HCN
43	680.2	50.7	2791	6	AAH18215	AAH18215 Human CDN
44	680.2	50.7	2791	6	AAH18213	AAH18213 Human CDN
45	680.2	50.7	2980	6	AAH18216	AAH18216 Human CDN

ALIGNMENTS

RESULT 1	AAZ09482	standard: DNA, 1342 BP.
ID	AAZ09482	standard: DNA, 1342 BP.
AC	AAZ09482	
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DT	02-NOV-1999	(first entry)
XX		
DE	Human Ih ion channel DNA fragment.	
XX		
KW	Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;	
KW	cardioactive; pacemaker; cardiac muscle; ion channel modulator;	
KW	treatment; diagnosis; ion channel-related disease; cardiac disease;	
KW	circulatory disorder; sinus ganglion regulation; sleep disorder;	
KW	cortico-thalamic neuron; pain; detection; mutation; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO942574-A1.	
XX		
PD	26-AUG-1999.	
XX		
PF	12-FEB-1999; 99WO-EP000942.	
XX		
PR	17-FEB-1998; 98DE-01006581.	
XX		
PA	(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.	
XX		
PI	Baumann A, Boenigk W, Gauss R, Scholten A, Seifert R, Kaupp B,	
XX		
DR	WPI, 1999-527472/44.	
XX		
PT	New nucleic acid encoding an Ih ion channel, used to identify specific	
PT	modulators, and for treatment, prevention and diagnosis of e.g. cardiac	
PT	disease.	
XX		
PS	Claim 3; Page 57; 82pp; German.	
XX		
CC	This invention describes a novel Ih ion channel, isolated from human, sea	
CC	urchin, bovine, rat, and fruitfly. The ion channels of the invention have	
CC	analgesic and cardioactive activity. The Ih ion channel participates in	
CC	the pacemaker function in cardiac muscle. The Ih ion channel nucleic acid	
CC	and its encoding protein is used to identify substances (A) that modulate	
CC	activity of ion channels, to treat and/or diagnose ion channel-related	

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OM nucleic - nucleic search, using sw model

Run on: January 4, 2005, 13:46:04 ; Search time 4568 Seconds
(without alignments)
10705.368 Million cell updates/sec

Title: US-09-640-582a-1
Perfect score: 1342
Sequence: 1 cgttcgcttcaccacgaatc.....cacctgchgcncctcacc 1342

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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1: gb_est1:*
2: gb_est2:*
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9: gb_gest2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1222.4	91.1	1794	3	BC039619 Homo sapi
2	736.8	54.9	913	6	CA488537 AGENCOURT
3	723.2	53.9	829	4	BI490383 603031868
4	719	53.6	3226	3	BC039156 Mus muscu
5	719	53.6	3265	3	AK032225 Mus muscu
6	719	53.6	4015	3	AK082719 Mus muscu
7	688.2	51.3	1620	9	AY399924 Homo sapi
8	687.4	51.2	815	2	BE546989 601071965
9	656.8	48.1	1638	9	AY399926 Mus muscu
10	646	48.1	786	4	BG974320 60284071
11	587	43.7	707	7	CK358214 AGENCOURT
12	585.2	43.6	691	2	AM073171 w994h02.x
13	541	40.3	564	6	CA842988 1t27f10.x
14	532.2	39.7	569	6	CB054837 NISC_gm06
15	532.2	39.7	569	6	CB054838 NISC_gm06
16	531.6	39.6	560	7	CK902966 1t27f10.y
17	527	39.3	595	2	BF593827 na05d02.x
18	526.6	39.2	568	1	AI809833 wh7f904.x
19	526	39.2	542	7	CK902965 1t27f10.x
20	523.6	39.0	659	6	CF253024 mdw004.b0
21	483	36.0	520	2	BF510959 UI-H-B14
22	473	35.2	957	6	BY714221 BY714221
23	471.4	35.1	1888	3	AK014722 Mus muscu
24	462.4	34.5	1120	5	BU956439 AGENCOURT

25	455.2	33.9	785	7	CN528592 UI-M-H00-
26	452.6	33.7	1620	9	AY399925 Pan trogl
27	451.8	33.7	780	2	BE260963 601151693
28	446.4	33.3	484	1	AI422949 ttf23a05.x
29	443.6	33.1	453	6	CA842473 1t27f10.y
30	438.6	32.7	509	1	AA843473 aj16b03.s
31	434.4	32.4	673	6	CB556893 AMGNNUC:N
32	433.8	32.3	954	6	CB8201579 AGENCOURT
33	429.8	32.0	702	7	CF531532 UI-M-FY0-
34	424.4	31.6	499	5	BK279829 BX279829
35	423.2	31.5	1087	2	BE798933 601583714
36	419.6	31.3	1263	9	AY401918 Mus muscu
37	416.8	31.1	858	4	BE793179 601581483
38	411.2	30.6	965	4	BI490063 603031868
39	411	30.6	785	5	BK872016 BX872016
40	403.4	30.1	974	5	BU914463 AGENCOURT
41	391.6	29.2	484	2	BE138253 UG50d03.Y
42	389.8	29.0	452	5	BK282916 BX282916
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44	379.2	28.3	1266	9	AY401917 Pan trogl
45	371.8	27.7	442	6	CB747868 AMGNNUC:N

ALIGNMENTS

RESULT 1
LOCUS BC039619
DEFINITION Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 2, mRNA (CDNA clone IMAGE:5730201).
ACCESSION BC039619
VERSION 1
KEYWORDS
SOURCE HTC
ORGANISM Homo sapiens (human)

REFERENCE
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